RAW SEQUENCE LISTING

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Application Serial Number: _____09/578, 669_____

Source: _____JFW016_____

Date Processed by STIC: _____12/20/2005_____

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IFW16

RAW SEQUENCE LISTING   DATE: 12/20/2005
PATENT APPLICATION: US/09/578,669   TIME: 12:32:19

Input Set : **N:\Crf3\RULE60\09578669.raw**
Output Set: **N:\CRF4\12202005\I578669.raw**

SEQUENCE LISTING
```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Grabstein, Kenneth
 6                    Paxton, Raymond
 7                    Pettit, Dean
10     (ii) TITLE OF INVENTION: Antagonists of IL-15
12    (iii) NUMBER OF SEQUENCES: 10
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Immunex Corporation
16          (B) STREET: 51 University Street
17          (C) CITY: Seattle
18          (D) STATE: Washington
19          (E) COUNTRY: USA
20          (F) ZIP: 98101
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Floppy disk
24          (B) COMPUTER: IBM PC Compatible
25          (C) OPERATING SYSTEM: Word for Windows 95, 7.0
26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28     (vi) CURRENT APPLICATION DATA:
```
C--> 29   **(A) APPLICATION NUMBER: US/09/578,669**
C--> 30   **(B) FILING DATE: 25-May-2000**
W--> 37   **(C) CLASSIFICATION: 536**
```
34    (vii) PRIOR APPLICATION DATA:
35          (A) APPLICATION NUMBER: US/08/392,317
36          (B) FILING DATE: 22 January, 1998
39   (viii) ATTORNEY/AGENT INFORMATION:
40          (A) NAME: Malaska, Stephen L.
41          (B) REGISTRATION NUMBER: 32,655
42          (C) REFERENCE/DOCKET NUMBER: 2831
44     (ix) TELECOMMUNICATION INFORMATION:
45          (A) TELEPHONE: 206-587-0430
48 (2) INFORMATION FOR SEQ ID NO: 1:
50      (i) SEQUENCE CHARACTERISTICS:
51          (A) LENGTH: 489 base pairs
52          (B) TYPE: nucleic acid
53          (C) STRANDEDNESS: single
54          (D) TOPOLOGY: linear
56     (ii) MOLECULE TYPE: cDNA
58    (iii) HYPOTHETICAL: NO
60     (iv) ANTI-SENSE: NO
63     (ix) FEATURE:
64          (A) NAME/KEY: CDS
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65            (B) LOCATION: 1..342
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71 ATG AGA ATT TCG AAA CCA CAT TTG AGA AGT ATT TCC ATC CAG TGC TAC        48
72 Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr
73  1           5                  10                  15
75 CTG TGT TTA CTT CTA AAG AGT CAT TTT CTA ACT GAA GCT GGC ATT CAT        96
76 Leu Cys Leu Leu Leu Lys Ser His Phe Leu Thr Glu Ala Gly Ile His
77             20                  25                  30
79 GTC TTC ATT TTG GGC TGT TTC AGT GCA GGG CTC CCT AAA ACA GAA GCC       144
80 Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
81             35                  40                  45
83 AAC TGG GTG AAT GTA ATA AGT GAT TTG AAA AAA ATT GAA GAT CTT ATT       192
84 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
85        50                  55                  60
87 CAA TCT ATG CAT ATT GAT GCT ACT TTA TAT ACA GAA AGT GAT GTT CAC       240
88 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
89 65                  70                  75                  80
91 CCC AGT TGC AAG GTA ACA GCA ATG AAG TGC TTT CTC TTG GAG TTG CAA       288
92 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
93             85                  90                  95
95 GTT ATT TCA CAT GAG TCC GGA GAT ACA GAT ATT CAT GAT ACA GTA GAA       336
96 Val Ile Ser His Glu Ser Gly Asp Thr Asp Ile His Asp Thr Val Glu
97        100                 105                 110
99 AAT CTT ATC ATC CTA GCA AAC AAC ATC TTG TCT TCT AAT GGG AAT ATA       384
100 Asn Leu Ile Ile Leu Ala Asn Asn Ile Leu Ser Ser Asn Gly Asn Ile
101        115                 120                 125
103 ACA GAA TCT GGA TGC AAA GAA TGT GAG GAA CTA GAG GAA AAA AAT ATT      432
104 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
105        130                 135                 140
107 AAA GAA TTT TTG CAG AGT TTT GTA CAT ATT GTC CAA ATG TTC ATC AAC      480
108 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
109 145                 150                 155                 160
111 ACT TCT TGA                                                         489
112 Thr Ser
116 (2) INFORMATION FOR SEQ ID NO: 2:
118      (i) SEQUENCE CHARACTERISTICS:
119          (A) LENGTH: 489 base pairs
120          (B) TYPE: nucleic acid
121          (C) STRANDEDNESS: single
122          (D) TOPOLOGY: linear
124     (ii) MOLECULE TYPE: cDNA
127     (ix) FEATURE:
128          (A) NAME/KEY: CDS
129          (B) LOCATION: 1..489
133     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
135 ATG AGA ATT TCG AAA CCA CAT TTG AGA AGT ATT TCC ATC CAG TGC TAC       48
136 Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr
137  1           5                  10                  15
139 TTG TGT TTA CTT CTA AAC AGT CAT TTT CTA ACT GAA GCT GGC ATT CAT       96
```

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140 Leu Cys Leu Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His
141             20                  25                  30
143 GTC TTC ATT TTG GGC TGT TTC AGT GCA GGG CTT CCT AAA ACA GAA GCC      144
144 Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
145             35                  40                  45
147 AAC TGG GTG AAT GTA ATA AGT GAT TTG AAA AAA ATT GAA GAT CTT ATT      192
148 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
149     50                  55                  60
151 CAA TCT ATG CAT ATT GAT GCT ACT TTA TAT ACG GAA AGT GAT GTT CAC      240
152 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
153 65                  70                  75                  80
155 CCC AGT TGC AAA GTA ACA GCA ATG AAG TGC TTT CTC TTG GAG TTA CAA      288
156 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
157                 85                  90                  95
159 GTT ATT TCA CTT GAG TCC GGA GAT GCA AGT ATT CAT GAT ACA GTA GAA      336
160 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
161             100                 105                 110
163 AAT CTG ATC ATC CTA GCA AAC AAC AGT TTG TCT TCT AAT GGG AAT GTA      384
164 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
165             115                 120                 125
167 ACA GAA TCT GGA TGC AAA GAA TGT GAG GAA CTG GAG GAA AAA AAT ATT      432
168 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
169     130                 135                 140
171 AAA GAA TTT TTG CAG AGT TTT GTA CAT ATT GTC CAA ATG TTC ATC AAC      480
172 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
173 145                 150                 155                 160
175 ACT TCT TGA                                                          489
176 Thr Ser
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179 (2) INFORMATION FOR SEQ ID NO: 3:
181   (i) SEQUENCE CHARACTERISTICS:
182   (A) LENGTH: 27 base pairs
183   (B) TYPE: nucleic acid
184   (C) STRANDEDNESS: single
185   (D) TOPOLOGY: linear
187   (ii) MOLECULE TYPE: cDNA
189   (iii) HYPOTHETICAL: NO
192   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
194 AATGTAATAA GTTGTTTGAA AAAAATT27
197 (2) INFORMATION FOR SEQ ID NO: 4:
199   (i) SEQUENCE CHARACTERISTICS:
200   (A) LENGTH: 27 base pairs
201   (B) TYPE: nucleic acid
202   (C) STRANDEDNESS: single
203   (D) TOPOLOGY: linear
205   (ii) MOLECULE TYPE: cDNA
207   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
209 AATGTAATAA GTTCTTTGAA AAAAATT27
212 (2) INFORMATION FOR SEQ ID NO: 5:
214   (i) SEQUENCE CHARACTERISTICS:

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215          (A) LENGTH: 24 base pairs
216          (B) TYPE: nucleic acid
217          (C) STRANDEDNESS: single
218          (D) TOPOLOGY: linear
220     (ii) MOLECULE TYPE: cDNA
222     (iii) HYPOTHETICAL: NO
224     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
226 GTTGATGAAC ATGCAGACAA TATG                                24
229 (2) INFORMATION FOR SEQ ID NO: 6:
231     (i) SEQUENCE CHARACTERISTICS:
232          (A) LENGTH: 24 base pairs
233          (B) TYPE: nucleic acid
234          (C) STRANDEDNESS: single
235          (D) TOPOLOGY: linear
237     (ii) MOLECULE TYPE: cDNA
239     (iii) HYPOTHETICAL: NO
241     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
243 GTTGATGAAC ATAGAGACAA TATG                                24
246 (2) INFORMATION FOR SEQ ID NO: 7:
248     (i) SEQUENCE CHARACTERISTICS:
249          (A) LENGTH: 39 base pairs
250          (B) TYPE: nucleic acid
251          (C) STRANDEDNESS: single
252          (D) TOPOLOGY: linear
254     (ii) MOLECULE TYPE: cDNA
256     (iii) HYPOTHETICAL: NO
258     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
260 GTCCTCGCAA CTAAGTCGAC TAACTGGGTG AATGTAATA39
263 (2) INFORMATION FOR SEQ ID NO: 8:
265     (i) SEQUENCE CHARACTERISTICS:
266          (A) LENGTH: 45 base pairs
267          (B) TYPE: nucleic acid
268          (C) STRANDEDNESS: single
269          (D) TOPOLOGY: linear
271     (ii) MOLECULE TYPE: cDNA
273     (iii) HYPOTHETICAL: NO
275     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
277 GAGTCATTCT CGACTTGCGG CCGCACCAGA AGTGTTGATG AACAT         45
280 (2) INFORMATION FOR SEQ ID NO: 9:
282     (i) SEQUENCE CHARACTERISTICS:
283          (A) LENGTH: 69 base pairs
284          (B) TYPE: nucleic acid
285          (C) STRANDEDNESS: single
286          (D) TOPOLOGY: linear
288     (ii) MOLECULE TYPE: cDNA
290     (iii) HYPOTHETICAL: NO
292     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
294 AATATGGTAC CTTTGGATAA AAGAGACTAC AAGGACGACG ATGACAAGAA    50
296 CTGGGTGAAT GTAATAAGT                                      69
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RAW SEQUENCE LISTING   DATE: 12/20/2005
PATENT APPLICATION: US/09/578,669   TIME: 12:32:19

            Input Set : N:\Crf3\RULE60\09578669.raw
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299 (2) INFORMATION FOR SEQ ID NO: 10:
301   (i) SEQUENCE CHARACTERISTICS:
302   (A) LENGTH: 36 base pairs
303   (B) TYPE: nucleic acid
304   (C) STRANDEDNESS: single
305   (D) TOPOLOGY: linear
307   (ii) MOLECULE TYPE: cDNA
309   (iii) HYPOTHETICAL: NO
311   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
313 GCGATATATC CATGGTCAAG AAGTGTTGAT GAACAT36

VERIFICATION SUMMARY   DATE: 12/20/2005
PATENT APPLICATION: **US/09/578,669**   TIME: 12:32:20

Input Set : **N:\Crf3\RULE60\09578669.raw**
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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)